Fluctuating Asymmetry in the Maxillary Sinus of Catarrhine Primates(III 共同利用研究 2.研究成果)

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（3）資料提供

資料1

Fluctuating Asymmetry in the Maxillary Sinus of Catarrhine Primates

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The paranasal sinuses exhibit considerable left-right asymmetry in size and shape. Although the maxillary sinus is subject to fewer variations than the other air cavities, little attention has been paid to the level of asymmetry in the maxillary sinus or to the variables associated with asymmetry. This knowledge, however, is of interest , because it has been suggested that an increase in fluctuating asymmetry (FA), i.e. a small random deviation from symmetry, may be an indicator of environmental and genomic stress [P.A. Parson, *Heredity* **68**, 361 (1992)].Volumes of the maxillary sinuses were obtained from serial coronal CT scans of a mixed-sex sample of skull from ten species of the genus *Macaca*, as well as of five hominoid species including man. Using the total skull length as a measure of body size, this study revealed that the absolute asymmetry in maxillary sinus volume increased with increasing skull size. However, there was no clear trend regarding the direction of asymmetry.To obtain an asymmetry pattern that is independent of skull size, an asymmetry index (AI) was calculated as the ratio of the larger sinus divided by the smaller sinus. A correlation analysis between AI and several cranial parameters revealed that the asymmetry in maxillary sinus size is largely independent from the skull architecture. Results suggest that the observed asymmetry pattern in maxillary sinus size can be considered as FA. However, more research is needed to evaluate whether the pattern of asymmetry in maxillary sinus size is indeed an useful indicator for increased environmental or genomic stress. This information might be obtained by studying the asymmetry pattern in case of congenital craniofacial malformations, because it has been suggested that cleft palates are associated with anomalies in the paranasal air sinuses.

資料2

ＦＩＳＨ法による霊長類染色体の比較研究

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蛍光 in situ ハイブリダイゼーション(FISH)法により、ヒトをはじめ霊長類各種の染色体を比較研究し、核型進化を調べることを本研究の目的とした。本年度は、大学院生笠井文生とともに、ヒト第２番染色体(HSA2)とそのチンパンジーにおける相同染色体である第12・13番染色体(PTR12・13)との比較を行なった。HSA2の長腕部は、セントロメア特異的反復配列であるアルフォイドDNAと染色体末端部特異的テロメア配列とを介在的に保有し、ヒト染色体の中でも特殊な構造を持つことで知られている。そこで、HSA2 由来のコスミド・クローン約60個をFISH 法によりマップし、両種の染色体のゲノム構成という視点から比較した。それによると、HSA2はPTR12とPTR13が短腕テロメア部で融合した形で対応する。この染色体再構成部位でのクローン配列に種差がみられなかった。このことから、両種の祖型染色体はPTR12とPTR13とに類似し、テロメア領域で融合しかつ一方のセントロメアが不活化したのがHSA2で、各々の染色体の短腕末端部のテロメア周辺に種特異的反復配列DNAを増幅させたのがPTR12とPTR13であると考えられる。他の染色体由来の DNA クローンを用い、多くの種につき同様の分析を行なえば、霊長類の詳細な染色体系統樹が構築できるものと考えられる。